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=> file medline caplus biosis scisearch embase biotechds
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                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.21       0.21

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FILE 'BIOTECHDS' ENTERED AT 13:13:32 ON 21 MAY 2003
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=> s 3-isopropylmate dehydratase
L1            0 3-ISOPROPYLMATE DEHYDRATASE

=> s 3-isopropylmalate dehydratase
L2           38 3-ISOPROPYLMALATE DEHYDRATASE

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3            33 DUP REM L2 (5 DUPLICATES REMOVED)

=> s l3 and corn
L4            1 L3 AND CORN

=> d l4

L4   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2003 ACS
AN   1999:297440  CAPLUS
DN   130:309229
TI   cDNAs for enzymes of branched-chain amino acid biosynthesis of crop plants
     and their uses
IN   Falco, Saverio Carl; Cahoon, Rebecca E.; Hitz, William D.; Kinney, Anthony
     J.; Rafalski, J. Antoni
PA   E.I. Du Pont De Nemours and Company, USA
SO   PCT Int. Appl., 102 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
PI   WO 9921880         A2   19990506       WO 1998-US22081  19981020
         W:  AL, AM, AU, AZ, BA, BB, BG, BR, BY, CA, CN, CU, CZ, EE, GD, GE,
             HR, HU, ID, IL, IS, JP, KG, KP, KR, KZ, LC, LK, LR, LT, LV, MD,
             MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, SL, TJ, TM, TR,
             TT, UA, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
             FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
             CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     US 6451581          B1   20020917       US 1998-173300   19981015
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     AU 9911909        A1   19990517       AU 1999-11909    19981020
     EP 1025210        A2   20000809       EP 1998-955005   19981020
        R:  DE, FR, GB
     BR 9815228        A    20010102       BR 1998-15228    19981020
     US 2002102715     A1   20020801       US 2001-27450    20011220
PRAI US 1997-63423P    P    19971028
     US 1998-173300    A3   19981015
     WO 1998-US22081   W    19981020


=> s l3 and 1990-1997/py
   5 FILES SEARCHED...
L5           9 L3 AND 1990-1997/PY

=> d l5 1-9 ibib ab

L5   ANSWER 1 OF 9     MEDLINE
ACCESSION NUMBER:   94227243     MEDLINE
DOCUMENT NUMBER:    94227243   PubMed ID: 8173074
TITLE:              The nucleotide sequence of genes involved in the leucine
                    biosynthetic pathway of Clostridium pasteurianum.
AUTHOR:             Oultram J D; Loughlin M; Walmsley R; Gunnery S M; Minton N
                    P
CORPORATE SOURCE:   Molecular Genetics Group, PHLS Centre for Applied
                    Microbiology and Research, Porton Down, Salisbury,
                    Wiltshire, UK.
SOURCE:             DNA SEQUENCE, (1993) 4 (2) 105-11.
                    Journal code: 9107800. ISSN: 1042-5179.
PUB. COUNTRY:       Switzerland
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
OTHER SOURCE:       GENBANK-L06666
ENTRY MONTH:        199406
ENTRY DATE:         Entered STN: 19940620
                    Last Updated on STN: 19940620
                    Entered Medline: 19940603
AB   A 2.2 kb SphI/ClaI fragment of the Clostridium pasteurianum chromosome has
     previously been cloned and shown to complement leuB401 and leuC171
     mutations in Escherichia coli. The nucleotide sequence of this fragment
     has been determined (2327 bp) and carries three open reading frames. The
     products of translation of these reading frames display significant
     homologies with the alpha-isopropylmalate isomerase subunit (leuD) gene of
     Salmonella typhimurium, the beta-isopropylmalate dehydrogenase (leuB)
     genes of several organisms, and the dihydroxyacid dehydrase (ilvD) gene of
     E. coli.

L5   ANSWER 2 OF 9     MEDLINE
ACCESSION NUMBER:   94171070     MEDLINE
DOCUMENT NUMBER:    94171070   PubMed ID: 8125330
TITLE:              The LEU1 gene of Ustilago maydis.
AUTHOR:             Rubin B P; Li D; Holloman W K
CORPORATE SOURCE:   Department of Microbiology, Cornell University Medical
                    College, New York, NY 10021.
CONTRACT NUMBER:    GM42482 (NIGMS)
     GM42548 (NIGMS)
SOURCE:             GENE, (1994 Mar 11) 140 (1) 131-5.
                    Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY:       Netherlands
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
OTHER SOURCE:       GENBANK-L20832
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ENTRY MONTH: 199404
ENTRY DATE: Entered STN: 19940420
Last Updated on STN: 19940420
Entered Medline: 19940414

AB The nucleotide sequence of the Ustilago maydis LEU1 gene has been determined. It contains a continuous open reading frame predicted to encode a protein of 773 amino acids with a molecular mass of 83,234 Da. The protein is homologous to alpha-isopropylmalate isomerases from prokaryotes and eukaryotes, as well as to other members of a family of structurally related isomerases.

L5 ANSWER 3 OF 9 MEDLINE
ACCESSION NUMBER: 94161495 MEDLINE
DOCUMENT NUMBER: 94161495 PubMed ID: 8117072
TITLE: Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis.
AUTHOR: Patek M; Krumbach K; Eggeling L; Sahm H
CORPORATE SOURCE: Institut fur Biotechnologie 1, Julich, Germany.
SOURCE: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, **(1994 Jan)** 60 (1) 133-40.
Journal code: 7605801. ISSN: 0099-2240.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X70959
ENTRY MONTH: 199403
ENTRY DATE: Entered STN: 19940406
Last Updated on STN: 19940406
Entered Medline: 19940328

AB Enzymes and genes of the isopropylmalate pathway leading to leucine in Corynebacterium glutamicum were studied, and assays were performed to unravel their connection to lysine oversynthesis. The first enzyme of the pathway is inhibited by leucine (Ki = 0.4 mM), and all three enzyme activities of the isopropylmalate pathway are reduced upon addition of this amino acid to the growth medium. Three different DNA fragments were cloned, each resulting in an oversynthesis of one of the three enzymes. The leuA complementing fragment encoding the isopropylmalate synthase was sequenced. The leuA gene is 1,848 bp in size, encoding a polypeptide with an M(r) of 68,187. Upstream of leuA there is extensive hyphenated dyad symmetry and a putative leader peptide, which are features characteristic of attenuation control. In addition to leuA, the sequenced fragment contains an open reading frame with high coding probability whose disruption did not result in a detectable phenotype. Furthermore, the sequence revealed that this open reading frame separates leuA from lysC, which encodes the aspartate kinase initiating the synthesis of all amino acids of the aspartate family. The leuA gene was inactivated in three lysine-secreting strains by insertional mutagenesis. Fermentations were performed, and a roughly 50% higher lysine yield was obtained when appropriate leucine concentrations limiting for growth of the constructed strains were used.

L5 ANSWER 4 OF 9 MEDLINE
ACCESSION NUMBER: 92224296 MEDLINE
DOCUMENT NUMBER: 92224296 PubMed ID: 1563047
TITLE: Heterologous transformation of Mucor circinelloides with the Phycomyces blakesleeanus leu1 gene.
AUTHOR: Iturriaga E A; Diaz-Minguez J M; Benito E P; Alvarez M I; Eslava A P
CORPORATE SOURCE: Departamento de Microbiologia y Genetica, Facultad de Biologia, Universidad de Salamanca, Spain.
SOURCE: CURRENT GENETICS, **(1992 Mar)** 21 (3) 215-23.

Journal code: 8004904. ISSN: 0172-8083.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199205
ENTRY DATE: Entered STN: 19920607
Last Updated on STN: 19920607
Entered Medline: 19920515

AB The leu1 gene of Phycomyces blakesleeanus was isolated within a HindIII-HindIII genomic DNA fragment by heterologous hybridization screening of a cosmid library, making use of the Mucor circinelloides leuA gene as a probe. The complete nucleotide sequence of this fragment reveals a single 2070 bp ORF with no introns, which presents at least 68% homology with that of the leuA gene. The P. blakesleeanus leu1 gene has also been expressed in the M. circinelloides mutant R7B (leu-), which was used to isolate the leuA gene by complementation. The homology with other known sequences shows that the leu1 gene encodes the P. blakesleeanus alpha-IPM (isopropylmalate) isomerase.

L5 ANSWER 5 OF 9 MEDLINE
ACCESSION NUMBER: 90272436 MEDLINE
DOCUMENT NUMBER: 90272436 PubMed ID: 2190189
TITLE: The nucleotide sequence of leuC from Salmonella typhimurium.
AUTHOR: Rosenthal E R; Calvo J M
CORPORATE SOURCE: Section of Biochemistry, Molecular and Cell Biology, Cornell University, Ithaca, NY 14853.
CONTRACT NUMBER: R01 GM38898 (NIGMS)
SOURCE: NUCLEIC ACIDS RESEARCH, **(1990 May 25)** 18 (10) 3072.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X51476
ENTRY MONTH: 199007
ENTRY DATE: Entered STN: 19900810
Last Updated on STN: 19900810
Entered Medline: 19900711

L5 ANSWER 6 OF 9 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 92279162 EMBASE
DOCUMENT NUMBER: 1992279162
TITLE: Isolation and prominent characteristics of an L-lysine hyperproducing strain of Corynebacterium glutamicum.
AUTHOR: Schrumpf B.; Eggeling L.; Sahm H.
CORPORATE SOURCE: Institut fur Biotechnologie, Forschungszentrum Julich GmbH, Postfach 1913,W-5170 Julich, Germany
SOURCE: Applied Microbiology and Biotechnology, (1992) 37/5 (566-571).
ISSN: 0175-7598 CODEN: AMBIDG
COUNTRY: Germany
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB A strain of Corynebacterium glutamicum was isolated that accumulated up to 44 g/l of L-lysine-HCl from 100 g/l of glucose x H2O in a simple mineral salts medium. This strain was obtained from the wild-type by two mutagenesis steps. In the first step the aminoethyl-cysteine-resistant strain MH20 was obtained and in the second step the Leu- derivative

MH20-22B. Enzymatic analysis of the hyperproducer MH20-22B revealed that this strain has feedback-resistant aspartate kinase and is devoid of isopropylmalate dehydratase. In addition, this strain has an extraordinarily high secretion rate of lysine (0.57 mmol/g dry weight and h), whereas strain MH20 has a low secretion rate (0.19 mmol/g per hour), and both strains have comparable cytosolic lysine concentrations. This suggests that the secretory step is influenced in the hyperproducer. Applying gene-directed mutagenesis, the aspartate kinase gene of the isolated strain (coding for feedback-resistant enzyme) was replaced by the gene coding of feedback-sensitive wild-type enzyme. The resulting strain still secretes lysine, although in low amounts (.ltoreq. 2 g/l). This is proof of the superior role of kinase regulation in metabolite flow and is indicative of unknown mutations, one of which is probably in the secretory system.

L5 ANSWER 7 OF 9 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 90053656 EMBASE
DOCUMENT NUMBER: 1990053656
TITLE: Yeast regulatory protein LEU3: A structure-function analysis.
AUTHOR: Zhou K.; Bai Y.; Kohlhaw G.B.
CORPORATE SOURCE: Department of Biochemistry, Purdue University, West Lafayette, IN 47907, United States
SOURCE: Nucleic Acids Research, (1990) 18/2 (291-298). ISSN: 0305-1048 CODEN: NARHAD
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Eleven mutations resulting in partially deleted or truncated LEU3 protein were generated by linker insertion or other modifications at restriction sites, deletion of restriction fragments, or oligonucleotide-directed mutagenesis. Functional studies of these mutants showed the following: (i) A sepcific DNA binding region is contained within the 173 N-terminal residues, but other regions of the protein are required for optimal binding. (ii) Activation of LEU2 expression depends on the C-terminal 113 residues of the LEU3 protein. (iii) Deletion of part or all of a central section of LEU3 eliminates the ability of the LEU3 protein to respond to the co-activator .alpha.-isopropylmalate, i.e. creates an unmodulated activator. (iv) Overproduction of unmodulated activator slows down cell growth. (v) Specific deletion of two short acidic regions, including one with net charge -19, has only minor effects on activation and modulation.

L5 ANSWER 8 OF 9 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1991-08933 BIOTECHDS
TITLE: Some properties of the leucine-biosynthesizing enzymes from Candida maltosa; 1-isopropylmalate-synthase, **3-isopropylmalate-dehydratase,** 3-isopropylmalate-dehydrogenase purification and characterization
AUTHOR: Bode R; Birnbaum D
LOCATION: Ernst-Moritz-Arndt-Universitaet Greifswald, Fachrichtung Biologie, Institut fuer Biochemie, Jahnstrasse 15a, O-2200 Greifswald, Germany.
SOURCE: J.Basic Microbiol.; (**1991**) 31, 1, 21-26 CODEN: JBMIEQ
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The enzymes of the leucine biosynthetic pathway in Candida maltosa L4 were partially purified and their catalytic properties determined. Maximum activity of the first enzyme, alpha-isopropylmalate

(IPM)-synthase (1-isopropylmalate-synthase, EC-4.1.3.12), was observed at pH values between 7.5 and 8.8. The Km values for alpha-ketoisovalerate and acetyl-CoA were 0.57 mM and 0.064 mM, respectively. Enzyme activity was inhibited specifically by L-leucine, and was strongly dependent on the presence of monovalent cations, preferably K+ (80 mM). IPM-dehydratase (**3-isopropylmalate-dehydratase**, EC-4.2.1.33) activity showed a sharp optimum at pH 8.5. The enzyme did not require cations for activity, and L-leucine, L-isoleucine and L-valine did not inhibit activity. The pH optimum of beta-IPM-dehydrogenase (3-isopropylmalate-dehydrogenase, EC-1.1.1.85) was 6.8, with 50% of the optimum activity expressed at pH 5.8 and pH 7.4. Monovalent cations were not required for dehydrogenase activity, but divalent ions increased activity (preferably Mn2+ at 1 mM). Enzyme activity was inhibited by L-valine. (23 ref)

L5 ANSWER 9 OF 9 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1991-05845 BIOTECHDS
TITLE: Production of alpha- and beta-isopropylmalate by a mutant from Candida maltosa; optimization of culture conditions
AUTHOR: Bode R; Samsonova I A; Birnbaum D
LOCATION: Institut fuer Biochemie, Fachrichtung Biologie, Ernst-Moritz-Arndt-Universitaet Greifswald, Jahnstrasse 15a, O-2200 Greifswald, Germany.
SOURCE: Zbl.Mikrobiol.; (**1991**) 146, 1, 35-39
CODEN: ZEMIDI
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Leucine-requiring mutants of Candida maltosa L4, obtained by nitrosoguanidine mutagenesis, and lacking 2-isopropylmalate-synthase (EC-4.1.3.12) (G630), **3-isopropylmalate-dehydratase** (EC-4.2.1.33) (G368) or 3-isopropylmalate-dehydrogenase (EC-1.1.1.85) (G587), were tested under growth-limiting concentrations of L-leucine for excretion of leucine-related biosynthesis intermediates. G368 and G587 excreted alpha-isopropylmalate (aIPM), and G587 produced high amounts of beta-isopropylmalate (bIPM). These intermediates were not produced by G630 or L4. In the presence of 20 g/l glucose, 5 g/l NH4H2PO4 and 75 mg/l L-leucine in a minimal salt medium, G587 produced about 900 mg/l bIPM during 72 hr of growth. The IPMs were extracted from the culture supernatant by ether extraction, sodium bicarbonate solution extraction, acidification, and further ether extraction. aIPM was obtained by taking up the ether extract in hot ethyl acetate and chloroform, standing overnight and filtration. bIPM was obtained from this filtrate by taking up evaporated residue in ether and n-heptane and slow evaporation. 1.4 g of bIPM was obtained from 3 l of culture broth. (12 ref)

=> s l3 and plant?
L6 4 L3 AND PLANT?

=> d l6 1-4 ibib ab

L6 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:634531 CAPLUS
DOCUMENT NUMBER: 136:258038
TITLE: Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021
AUTHOR(S): Capela, Delphine; Barloy-Hubler, Frederique; Gouzy, Jerome; Bothe, Gordana; Ampe, Frederic; Batut, Jacques; Boistard, Pierre; Becker, Anke; Boutry, Marc; Cadieu, Edouard; Dreano, Stephane; Gloux, Stephanie; Godrie, Therese; Goffeau, Andre; Kahn, Daniel; Kiss,

Erno; Lelaure, Valerie; Masuy, David; Pohl, Thomas; Portetelle, Daniel; Puhler, Alfred; Purnelle, Benedicte; Ramsperger, Ulf; Renard, Clotilde; Thebault, Patricia; Vandenbol, Micheline; Weidner, Stefan; Galibert, Francis

CORPORATE SOURCE: Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, Unite Mixte de Recherche (UMR) 215 Centre National de la Recherche Scientifique (CNRS), Institut National de la Recherche Agronomique, Chemin, Tolosan, F-31326, Fr.

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2001), 98(17), 9877-9882
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Sinorhizobium meliloti is an .alpha.-proteobacterium that forms agronomically important N2-fixing root nodules in legumes. We report here the complete sequence of the largest constituent of its genome, a 62.7% GC-rich 3654,135-bp circular chromosome. Annotation allowed assignment of a function to 59% of the 3341 predicted protein-coding ORFs, the rest exhibiting partial, weak, or no similarity with any known sequence. Unexpectedly, the level of reiteration within this replicon is low, with only two genes duplicated with more than 90% nucleotide sequence identity, transposon elements accounting for 2.2% of the sequence, and a few hundred short repeated palindromic motifs (RIME1, RIME2, and C) widespread over the chromosome. Three regions with a significantly lower GC content are most likely of external origin. Detailed annotation revealed that this replicon contains all housekeeping genes except two essential genes that are located on pSymB. Amino acid/peptide transport and degrdn. and sugar metab. appear as two major features of the S. meliloti chromosome. The presence in this replicon of a large no. of nucleotide cyclases with a peculiar structure, as well as of genes homologous to virulence determinants of animal and **plant** pathogens, opens perspectives in the study of this bacterium both as a free-living soil microorganism and as a **plant** symbiont.

REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:312014 CAPLUS
DOCUMENT NUMBER: 136:64938

TITLE: Toward elucidating the global gene expression patterns of developing Arabidopsis: parallel analysis of 8 300 genes by a high-density oligonucleotide probe array

AUTHOR(S): Zhu, Tong; Budworth, Paul; Han, Bin; Brown, Devon; Chang, Hur-Song; Zou, Guangzhou; Wang, Xun

CORPORATE SOURCE: Torrey Mesa Research Institute, Inc., San Diego, CA, 92121, USA

SOURCE: Plant Physiology and Biochemistry (Paris, France) (2001), 39(3-4), 221-242
CODEN: PPBIEX; ISSN: 0981-9428

PUBLISHER: Editions Scientifiques et Medicales Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Arabidopsis thaliana has been widely used as a model system, in various aspects of biol. studies, such as genomics, genetics, cellular, developmental and mol. biol. In order to reveal the mol. events and regulatory networks controlling Arabidopsis development and responses to genetic and environmental changes, we designed and used a high-d. oligonucleotide probe array (GeneChip) to profile global gene expression patterns. The Arabidopsis oligonucleotide probe array consists of probes from 8 300 unique Arabidopsis genes, which covers approx. one-third of the

genome. Global transcription profiles of A. thaliana in various developmental stages, and their responses to different environments were generated using this microarray, and archived. Here, we analyze data sets derived from nineteen independent expts. Constitutively and differentially expressed genes in seedlings, roots, leaves, inflorescences, flowers and siliques at different developmental stages were identified. Functions of these genes based on homologs were detd. and categorized. Our results provide insight into the coordinated transcriptional regulation of the genes during **plant** growth and development.

REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:577179 CAPLUS
DOCUMENT NUMBER: 131:225907
TITLE: Cross-species characterization of abundantly expressed Ochrobactrum anthropi gene products
AUTHOR(S): Wasinger, Valerie, C.; Urquhart, Brooke L.; Humphery-Smith, Ian
CORPORATE SOURCE: Center Proteome Research Gene-Product Mapping, Univ. Sydney, Eveleigh, Australia
SOURCE: Electrophoresis (1999), 20(11), 2196-2203
CODEN: ELCTDN; ISSN: 0173-0835
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The identity of 45 protein spots representing 32 orthologs within the Ochrobactrum anthropi proteome within a gradient of pH 4-7, and mass range 5-90 kDa were detd. across species boundaries. These proteins could be classified into 13 functional categories and establish metabolic, regulatory and translatory systems including amino acid biosynthesis, electron transport and the potential for **plant** symbiosis in a molecularly understudied organism. Amino acid compn. and/or peptide mass fingerprinting were employed as a means to search the Swiss-Prot and OWL protein sequence databases for similarity within a broad taxonomic class of bacteria. Candidate matches from database searches could be compared and a simple multiplication matrix based27 on co-occurrence and rank within the top 96 most similar entries was used to provide statistical confidence. This math. matrix was evaluated with respect to the characterization of O. anthropi, an unsequenced and understudied bacterium, in the light of the recent influx of DNA sequence information.
REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:297440 CAPLUS
DOCUMENT NUMBER: 130:309229
TITLE: cDNAs for enzymes of branched-chain amino acid biosynthesis of crop **plants** and their uses
INVENTOR(S): Falco, Saverio Carl; Cahoon, Rebecca E.; Hitz, William D.; Kinney, Anthony J.; Rafalski, J. Antoni
PATENT ASSIGNEE(S): E.I. Du Pont De Nemours and Company, USA
SOURCE: PCT Int. Appl., 102 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9921880	A2	19990506	WO 1998-US22081	19981020

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            MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, SL, TJ, TM, TR,
            TT, UA, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
        RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
            FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
            CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
    US 6451581        B1   20020917       US 1998-173300   19981015
    AU 9911909        A1   19990517       AU 1999-11909    19981020
    EP 1025210        A2   20000809       EP 1998-955005   19981020
        R:  DE, FR, GB
    BR 9815228        A    20010102       BR 1998-15228    19981020
    US 2002102715     A1   20020801       US 2001-27450    20011220
PRIORITY APPLN. INFO.:                   US 1997-63423P   P  19971028
                                         US 1998-173300   A3 19981015
                                         WO 1998-US22081  W  19981020
AB   Plant genes for enzymes of branched-chain amino acid
     biosynthesis of crop plants (corn, wheat, rice, soybean) are
     cloned and characterized for use in alteration of patterns of
     branched-chain amino acid biosynthesis and accumulation.  The genes were
     identified by BLAST searching of EST banks from a no. of plants
     and tissues.


=> d his

     (FILE 'HOME' ENTERED AT 13:12:51 ON 21 MAY 2003)

     FILE 'MEDLINE, CAPLUS, BIOSIS, SCISEARCH, EMBASE, BIOTECHDS' ENTERED AT
     13:13:32 ON 21 MAY 2003
L1             0 S 3-ISOPROPYLMATE DEHYDRATASE
L2            38 S 3-ISOPROPYLMALATE DEHYDRATASE
L3            33 DUP REM L2 (5 DUPLICATES REMOVED)
L4             1 S L3 AND CORN
L5             9 S L3 AND 1990-1997/PY
L6             4 S L3 AND PLANT?

=> log y
COST IN U.S. DOLLARS                          SINCE FILE      TOTAL
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FULL ESTIMATED COST                              44.18      44.39

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)    SINCE FILE      TOTAL
                                                 ENTRY    SESSION
CA SUBSCRIBER PRICE                              -2.60      -2.60

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☐ 1. Document ID: US 20020197605 A1

L1: Entry 1 of 17 File: PGPB Dec 26, 2002

PGPUB-DOCUMENT-NUMBER: 20020197605
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020197605 A1

TITLE: Novel Polynucleotides

PUBLICATION-DATE: December 26, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Nakagawa, Satoshi	Tokyo		JP	
Mizoguchi, Hiroshi	Tokyo		JP	
Ando, Seiko	Tokyo		JP	
Hayashi, Mikiro	Tokyo		JP	
Ochiai, Keiko	Tokyo		JP	
Yokoi, Haruhiko	Tokyo		JP	
Tateishi, Naoko	Tokyo		JP	
Senoh, Akihiro	Tokyo		JP	
Ikeda, Masato	Tokyo		JP	
Ozaki, Akio	Hofu-shi		JP	

US-CL-CURRENT: 435/6; 435/287.2, 435/91.2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Desc | Image

☐ 2. Document ID: US 20020102715 A1

L1: Entry 2 of 17 File: PGPB Aug 1, 2002

PGPUB-DOCUMENT-NUMBER: 20020102715
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020102715 A1

TITLE: Plant branched-chain amino acid biosynthetic enzymes

PUBLICATION-DATE: August 1, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Falco, Saverio Carl	Arden	DE	US	
Cahoon, Rebecca E.	Wilmington	DE	US	

US-CL-CURRENT: 435/252.3; 435/190, 435/320.1, 435/410, 435/69.1, 536/23.2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

☐ 3. Document ID: US 20020082234 A1

L1: Entry 3 of 17 File: PGPB Jun 27, 2002

PGPUB-DOCUMENT-NUMBER: 20020082234
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020082234 A1

TITLE: Novel prokaryotic polynucleotides, polypeptides and their uses

PUBLICATION-DATE: June 27, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Black, Michael Terence	Le Vesinet	PA	FR	
Hodgson, John Edward	Paris	PA	FR	
Knowles, David Justin Charles	Boroughbridge	PA	GB	
Reichard, Raymond Winfield	Quakertown	PA	US	
Nicholas, Richard O.	Collegeville	PA	US	
Burnham, Martin Karl Russel	Barto		US	
Pratt, Julie M.	Wigston Leicester		GB	
Rosenberg, Martin	Royersford		US	
Ward, Judith M.	Dorking Surrey		GB	
Lonetto, Michael Arthur	Collegeville		US	

US-CL-CURRENT: 514/44; 424/130.1, 514/12

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

☐ 4. Document ID: US 20020040490 A1

L1: Entry 4 of 17 File: PGPB Apr 4, 2002

PGPUB-DOCUMENT-NUMBER: 20020040490
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020040490 A1

TITLE: Expressed sequences of arabidopsis thaliana

PUBLICATION-DATE: April 4, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Gorlach, Jorn	Durham	NC	US	
An, Yong-Qiang	San Diego	CA	US	
Hamilton, Carol M.	Apex	NC	US	
Price, Jennifer L.	Raleigh	NC	US	
Raines, Tracy M.	Durham	NC	US	
Yu, Yang	Martinsville	NJ	US	
Rameaka, Joshua G.	Durham	NC	US	
Page, Amy	Durham	NC	US	
Mathew, Abraham V.	Cary	NC	US	
Ledford, Brooke L.	Holly Springs	NC	US	
Woessner, Jeffrey P.	Hillsborough	NC	US	
Haas, William David	Durham	NC	US	
Garcia, Carlos A.	Carrboro	NC	US	
Kricker, Maja	Pittsboro	NC	US	
Slater, Ted	Apex	NC	US	
Davis, Keith R.	Durham	NC	US	
Allen, Keith	Cary	NC	US	
Hoffman, Neil	Chapel Hill	NC	US	
Hurban, Patrick	Raleigh	NC	US	

US-CL-CURRENT: 800/288; 435/4, 536/23.2, 536/23.6

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw. Desc | Image

☐ 5. Document ID: US 6528289 B1

L1: Entry 5 of 17 File: USPT Mar 4, 2003

US-PAT-NO: 6528289
DOCUMENT-IDENTIFIER: US 6528289 B1

TITLE: Nucleotide sequence of the Haemophilus influenzae Rd genome, fragments thereof, and uses thereof

DATE-ISSUED: March 4, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Fleischmann; Robert D.	Gaithersburg	MD		
Adams; Mark D.	N. Potomac	MD		
White; Owen	Gaithersburg	MD		
Smith; Hamilton O.	Towson	MD		
Venter; J. Craig	Potomac	MD		

US-CL-CURRENT: 435/91.41; 435/252.3, 435/320.1, 435/6, 536/23.1, 536/23.7

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw. Desc | Image

☐ 6. Document ID: US 6506581 B1

L1: Entry 6 of 17 File: USPT Jan 14, 2003

US-PAT-NO: 6506581
DOCUMENT-IDENTIFIER: US 6506581 B1

TITLE: Nucleotide sequence of the Haemophilus influenzae Rd genome, fragments thereof, and uses thereof

DATE-ISSUED: January 14, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Fleischmann; Robert D.	Gaithersburg	MD		
Adams; Mark D.	N. Potomac	MD		
White; Owen	Gaithersburg	MD		
Smith; Hamilton O.	Towson	MD		
Venter; J. Craig	Potomac	MD		

US-CL-CURRENT: 435/69.1; 435/252.3, 435/320.1, 435/69.3, 435/91.41, 536/23.7

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw. Desc | Image

☐ 7. Document ID: US 6503729 B1

L1: Entry 7 of 17 File: USPT Jan 7, 2003

US-PAT-NO: 6503729
DOCUMENT-IDENTIFIER: US 6503729 B1

TITLE: Selected polynucleotide and polypeptide sequences of the methanogenic archaeon, methanococcus jannashii

DATE-ISSUED: January 7, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bult; Carol J.	Bar Harbor	ME		
White; Owen R.	Gaithersburg	MD		
Smith; Hamilton O.	Baltimore	MD		
Woese; Carl R.	Urbana	IL		
Venter; J. Craig	Rockville	MD		

US-CL-CURRENT: 435/69.1; 435/252.3, 435/320.1, 435/325, 536/23.1, 536/23.5

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw. Desc | Image

☐ 8. Document ID: US 6451581 B1

L1: Entry 8 of 17 File: USPT Sep 17, 2002

US-PAT-NO: 6451581
DOCUMENT-IDENTIFIER: US 6451581 B1

TITLE: Plant branched-chain amino acid biosynthetic enzymes

DATE-ISSUED: September 17, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Falco; Saverio Carl	Arden	DE		
Cahoon; Rebecca E.	Greenville	DE		
Hitz; William D.	Wilmington	DE		
Kinney; Anthony J.	Wilmington	DE		
Rafalski; J. Antoni	Wilmington	DE		

US-CL-CURRENT: 435/252.3; 435/232, 435/255.1, 435/320.1, 435/419, 435/468, 435/948, 530/350, 536/23.2, 800/278, 800/295

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 9. Document ID: US 6355450 B1

L1: Entry 9 of 17 File: USPT Mar 12, 2002

US-PAT-NO: 6355450
DOCUMENT-IDENTIFIER: US 6355450 B1

TITLE: Computer readable genomic sequence of Haemophilus influenzae Rd, fragments thereof, and uses thereof

DATE-ISSUED: March 12, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Fleischmann; Robert D.	Gaithersburg	MD		
Adams; Mark D.	N. Potomac	MD		
White; Owen	Gaithersburg	MD		
Smith; Hamilton O.	Towson	MD		
Venter; J. Craig	Potomac	MD		

US-CL-CURRENT: 435/69.1; 435/252.3, 435/320.1, 435/851, 536/23.1, 536/23.7, 536/24.32, 536/24.33

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 10. Document ID: US 6348582 B1

L1: Entry 10 of 17 File: USPT Feb 19, 2002

US-PAT-NO: 6348582
DOCUMENT-IDENTIFIER: US 6348582 B1

TITLE: Prokaryotic polynucleotides polypeptides and their uses

DATE-ISSUED: February 19, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Black; Michael Terence	Le Vesinet			FR
Hodgson; John Edward	Paris			FR
Knowles; David Justin Charles	Boroughbridge			GB
Reichard; Raymond Winfield	Quakertown	PA		
Nicholas; Richard O	Collegeville	PA		
Burnham; Martin Karl Russel	Barto	PA		
Pratt; Julie M	Wigston Leicester			GB
Rosenberg; Martin	Royersford	PA		
Ward; Judith M	Dorking			GB
Lonetto; Michael Arthur	Collegeville	PA		

US-CL-CURRENT: 536/23.1; 424/185.1, 435/252.3, 435/320.1, 435/69.1, 530/350, 536/22.1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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Terms	Documents
3-isopropylmalate dehydratase	17

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L1: Entry 8 of 17 File: USPT Sep 17, 2002

US-PAT-NO: 6451581
DOCUMENT-IDENTIFIER: US 6451581 B1

TITLE: Plant branched-chain amino acid biosynthetic enzymes

DATE-ISSUED: September 17, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Falco; Saverio Carl	Arden	DE		
Cahoon; Rebecca E.	Greenville	DE		
Hitz; William D.	Wilmington	DE		
Kinney; Anthony J.	Wilmington	DE		
Rafalski; J. Antoni	Wilmington	DE		

US-CL-CURRENT: 435/252.3; 435/232, 435/255.1, 435/320.1, 435/419, 435/468, 435/948, 530/350, 536/23.2, 800/278, 800/295

CLAIMS:

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence that encodes a dihydroxyacid dehydratase polypeptide, wherein said nucleotide sequence has a sequence identity of at least 80% based on the Clustal method of alignment when compared to a polynucleotide selected from the group consisting of SEQ ID NOs:1, 3, and 5.

2. The polynucleotide of claim 1 wherein the sequence identity is at least 85%.

3. The polynucleotide of claim 1 wherein the sequence identity is at least 90%.

4. The polynucleotide of claim 1 wherein the sequence identity is at least 95%.

5. The polynucleotide of claim 1 wherein the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NOs:2, 4, and 6.

6. The polynucleotide of claim 1, wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3, and 5.

7. An isolated complement of the polynucleotide of claim 1, wherein (a) the complement and the polynucleotide consist of the same number of nucleotides, and (b) the nucleotide sequences of the complement and the polynucleotide have 100% complementarity.

8. A recombinant DNA construct comprising the polynucleotide of claim 1 operably linked to at least one suitable regulatory sequence.

9. A cell comprising the polynucleotide of claim 1.

10. The cell of claim 9, wherein the cell is selected from the group consisting of a yeast cell, a bacterial cell and a plant cell.

11. A virus comprising the polynucleotide of claim 1.

12. A transgenic plant comprising the polynucleotide of claim 1.

WEST Search History

DATE: Wednesday, May 21, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ			
L3	L2 and dna	6	L3
L2	L1 and corn	6	L2
L1	3-isopropylmalate dehydratase	17	L1

END OF SEARCH HISTORY